

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 09/744,847A
Source: IFWJ0
Date Processed by STIC: 2/23/06

ENTERED



IFWO

RAW SEQUENCE LISTING

DATE: 02/23/2006

PATENT APPLICATION: US/09/744,847A

TIME: 15:00:42

Input Set : E:\2618-102-PUS.ST25.txt

Output Set: N:\CRF4\02232006\I744847A.raw

3 <110> APPLICANT: Sim, Gek-Kee
 4 Dreitz, Matthew J.
 6 <120> TITLE OF INVENTION: T CELL RECEPTOR PROTEINS, NUCLEIC ACID MOLECULES, AND USES
 7 THEREOF
 9 <130> FILE REFERENCE: 2618-102-PUS
 11 <140> CURRENT APPLICATION NUMBER: 09/744,847A
 12 <141> CURRENT FILING DATE: 2001-01-29
 14 <150> PRIOR APPLICATION NUMBER: PCT/US99/17309
 15 <151> PRIOR FILING DATE: 1999-07-29
 17 <150> PRIOR APPLICATION NUMBER: 60/094,506
 18 <151> PRIOR FILING DATE: 1998-07-29
 20 <160> NUMBER OF SEQ ID NOS: 111
 22 <170> SOFTWARE: PatentIn version 3.3
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 381
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Canis familiaris
 30 <220> FEATURE:
 31 <221> NAME/KEY: CDS
 32 <222> LOCATION: (1)..(381)
 34 <400> SEQUENCE: 1

35 atc gga ctc ctc tgt ggt gtg gcc ttt tgt ttc ctg gga gta ggc ctt	48
36 ile gly leu leu cys gly val ala phe cys phe leu gly val gly leu	
37 1 5 10 15	
39 ttg aac gca caa gtg act caa acc ccg aga caa ctc atc aaa aaa gtg	96
40 leu asn ala gln val thr gln thr pro arg gln leu ile lys lys val	
41 20 25 30	
43 gga gcg aaa gtt ttg ttg aaa tgt tca cag aat atg gac cat gaa aga	144
44 gly ala lys val leu leu lys cys ser gln asn met asp his glu arg	
45 35 40 45	
47 atg ttc tgg tat cga caa gac cca ggt ctg ggg ttg cgg ctg ctc tac	192
48 met phe trp tyr arg gln asp pro gly leu gly leu arg leu leu tyr	
49 50 55 60	
51 tgg tcc tat aat att gac agt gtt gag aca gga gac atc cct tat ggg	240
52 trp ser tyr asn ile asp ser val glu thr gly asp ile pro tyr gly	
53 65 70 75 80	
55 tac agt gtc tcg agg aag aag aag gat gcc ttc ccc ttg att ctg gag	288
56 tyr ser val ser arg lys lys lys asp ala phe pro leu ile leu glu	
57 85 90 95	
59 tct gct cgc atc aac cag aca tct gtg tac ttc tgc gcc agc agc ccg	336
60 ser ala arg ile asn gln thr ser val tyr phe cys ala ser ser pro	
61 100 105 110	
63 ttt agc caa aat acc cag tac ttc ggg gcg ggc acc cgg ctg cta	381

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64 Phe Ser Gln Asn Thr Gln Tyr Phe Gly Ala Gly Thr Arg Leu Leu
65      115      120      125
68 <210> SEQ ID NO: 2
69 <211> LENGTH: 127
70 <212> TYPE: PRT
71 <213> ORGANISM: Canis familiaris
73 <400> SEQUENCE: 2
75 Ile Gly Leu Leu Cys Gly Val Ala Phe Cys Phe Leu Gly Val Gly Leu
76 1      5      10      15
79 Leu Asn Ala Gln Val Thr Gln Thr Pro Arg Gln Leu Ile Lys Lys Val
80      20      25      30
83 Gly Ala Lys Val Leu Leu Lys Cys Ser Gln Asn Met Asp His Glu Arg
84      35      40      45
87 Met Phe Trp Tyr Arg Gln Asp Pro Gly Leu Gly Leu Arg Leu Leu Tyr
88      50      55      60
91 Trp Ser Tyr Asn Ile Asp Ser Val Glu Thr Gly Asp Ile Pro Tyr Gly
92 65      70      75      80
95 Tyr Ser Val Ser Arg Lys Lys Lys Asp Ala Phe Pro Leu Ile Leu Glu
96      85      90      95
99 Ser Ala Arg Ile Asn Gln Thr Ser Val Tyr Phe Cys Ala Ser Ser Pro
100      100      105      110
103 Phe Ser Gln Asn Thr Gln Tyr Phe Gly Ala Gly Thr Arg Leu Leu
104      115      120      125
107 <210> SEQ ID NO: 3
108 <211> LENGTH: 381
109 <212> TYPE: DNA
110 <213> ORGANISM: Canis familiaris
112 <400> SEQUENCE: 3
113 tagcagccgg gtgcccgcgc cgaagtactg ggtatttttg ctaaaccgggc tactggcgca      60
115 gaagtacaca gatgtctggg tgatgcgagc agactccaga atcaagggga aggcacctt      120
117 cttcttctctc gagacactgt acccataagg gatgtctcct gtctcaacac tgtcaatatt      180
119 ataggaccag tagagcagcc gcaacccccag acctgggtct tgtcgatacc agaacattct      240
121 ttcattgggtc atattctgtg aacatttcaa caaaactttc gctcccactt ttttgatgag      300
123 ttgtctcggg gtttgagtca cttgtgcgtt caaaaggcct actcccagga aacaaaaggc      360
125 cacaccacag aggagtccga t                                     381
128 <210> SEQ ID NO: 4
129 <211> LENGTH: 408
130 <212> TYPE: DNA
131 <213> ORGANISM: Canis familiaris
134 <220> FEATURE:
135 <221> NAME/KEY: CDS
136 <222> LOCATION: (25)..(408)
138 <400> SEQUENCE: 4
139 acggtgaagg gctagcacct aaag atg ctg act tgc ctg cta ctc ctc ctg      51
140      Met Leu Thr Cys Leu Leu Leu Leu
141      1      5
143 gga caa ggc tct gtg ttt gga gct ctt gtc tct caa aag ccg cgc agg      99
144 Gly Gln Gly Ser Val Phe Gly Ala Leu Val Ser Gln Lys Pro Arg Arg
145 10      15      20      25

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147 gac atc tgt caa cgt ggg acc tcc att acc atc cac tgt gag gtc gat      147
148 Asp Ile Cys Gln Arg Gly Thr Ser Ile Thr Ile His Cys Glu Val Asp
149          30          35          40
151 acc caa gtc acc ttg atg ttc tgg tac cgt cag ctc cca gga cag agc      195
152 Thr Gln Val Thr Leu Met Phe Trp Tyr Arg Gln Leu Pro Gly Gln Ser
153          45          50          55
155 ttg ata ctg att gca acc gca aac cag ggt gca gag gcc acc tac gaa      243
156 Leu Ile Leu Ile Ala Thr Ala Asn Gln Gly Ala Glu Ala Thr Tyr Glu
157          60          65          70
159 agt gga ttt acc agg gag aag ttt ccc atc agc cgc cga acc cta atg      291
160 Ser Gly Phe Thr Arg Glu Lys Phe Pro Ile Ser Arg Arg Thr Leu Met
161          75          80          85
163 ttc tcc act ctg act gtg agc aac ctg agc ctc gaa gac acc agc tct      339
164 Phe Ser Thr Leu Thr Val Ser Asn Leu Ser Leu Glu Asp Thr Ser Ser
165 90          95          100          105
167 tac ttc tgc agc att tgg tac ggg gag ggg gag cag cac ttt ggg cca      387
168 Tyr Phe Cys Ser Ile Trp Tyr Gly Glu Gly Glu Gln His Phe Gly Pro
169          110          115          120
171 ggg acc cgg ctc acc gtc cta      408
172 Gly Thr Arg Leu Thr Val Leu
173          125
176 <210> SEQ ID NO: 5
177 <211> LENGTH: 128
178 <212> TYPE: PRT
179 <213> ORGANISM: Canis familiaris
181 <400> SEQUENCE: 5
183 Met Leu Thr Cys Leu Leu Leu Leu Gly Gln Gly Ser Val Phe Gly
184 1          5          10          15
187 Ala Leu Val Ser Gln Lys Pro Arg Arg Asp Ile Cys Gln Arg Gly Thr
188          20          25          30
191 Ser Ile Thr Ile His Cys Glu Val Asp Thr Gln Val Thr Leu Met Phe
192          35          40          45
195 Trp Tyr Arg Gln Leu Pro Gly Gln Ser Leu Ile Leu Ile Ala Thr Ala
196          50          55          60
199 Asn Gln Gly Ala Glu Ala Thr Tyr Glu Ser Gly Phe Thr Arg Glu Lys
200 65          70          75          80
203 Phe Pro Ile Ser Arg Arg Thr Leu Met Phe Ser Thr Leu Thr Val Ser
204          85          90          95
207 Asn Leu Ser Leu Glu Asp Thr Ser Ser Tyr Phe Cys Ser Ile Trp Tyr
208          100          105          110
211 Gly Glu Gly Glu Gln His Phe Gly Pro Gly Thr Arg Leu Thr Val Leu
212          115          120          125
215 <210> SEQ ID NO: 6
216 <211> LENGTH: 408
217 <212> TYPE: DNA
218 <213> ORGANISM: Canis familiaris
220 <400> SEQUENCE: 6
221 taggacggtg agccgggtcc ctggcccaaa gtgctgctcc cccctcccgt accaaatgct      60
223 gcagaagtaa gagctggtgt cttcgaggct caggttgctc acagtcagag tggagaacat      120

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225 taggggttcgg cggctgatgg gaaacttctc cctggtaaata ccactttcgt aggtggcctc 180
227 tgcaccctgg tttgcggttg caatcagtat caagctctgt cctgggagct gacggtacca 240
229 gaacatcaag gtgacttggg tatcgacctc acagtggatg gtaatggagg tcccacgttg 300
231 acagatgtcc ctgcgcggct tttgagagac aagagctcca aacacagagc cttgtcccag 360
233 gaggagtagc aggcaagtca gcatctttag gtgctagccc ttcaccgt 408
236 <210> SEQ ID NO: 7
237 <211> LENGTH: 384
238 <212> TYPE: DNA
239 <213> ORGANISM: Canis familiaris
242 <220> FEATURE:
243 <221> NAME/KEY: exon
244 <222> LOCATION: (1)..(384)
246 <400> SEQUENCE: 7
247 atg ctg act tgc ctg cta ctc ctc ctg gga caa ggc tct gtg ttt gga 48
248 Met Leu Thr Cys Leu Leu Leu Leu Leu Gly Gln Gly Ser Val Phe Gly
249 1 5 10 15
251 gct ctt gtc tct caa aag ccg cgc agg gac atc tgt caa cgt ggg acc 96
252 Ala Leu Val Ser Gln Lys Pro Arg Arg Asp Ile Cys Gln Arg Gly Thr
253 20 25 30
255 tcc att acc atc cac tgt gag gtc gat acc caa gtc acc ttg atg ttc 144
256 Ser Ile Thr Ile His Cys Glu Val Asp Thr Gln Val Thr Leu Met Phe
257 35 40 45
259 tgg tac cgt cag ctc cca gga cag agc ttg ata ctg att gca acc gca 192
260 Trp Tyr Arg Gln Leu Pro Gly Gln Ser Leu Ile Leu Ile Ala Thr Ala
261 50 55 60
263 aac cag ggt gca gag gcc acc tac gaa agt gga ttt acc agg gag aag 240
264 Asn Gln Gly Ala Glu Ala Thr Tyr Glu Ser Gly Phe Thr Arg Glu Lys
265 65 70 75 80
267 ttt ccc atc agc cgc cga acc cta atg ttc tcc act ctg act gtg agc 288
268 Phe Pro Ile Ser Arg Arg Thr Leu Met Phe Ser Thr Leu Thr Val Ser
269 85 90 95
271 aac ctg agc ctc gaa gac acc agc tct tac ttc tgc agc att tgg tac 336
272 Asn Leu Ser Leu Glu Asp Thr Ser Ser Tyr Phe Cys Ser Ile Trp Tyr
273 100 105 110
275 ggg gag ggg gag cag cac ttt ggg cca ggg acc cgg ctc acc gtc cta 384
276 Gly Glu Gly Glu Gln His Phe Gly Pro Gly Thr Arg Leu Thr Val Leu
277 115 120 125
280 <210> SEQ ID NO: 8
281 <211> LENGTH: 384
282 <212> TYPE: DNA
283 <213> ORGANISM: Canis familiaris
285 <400> SEQUENCE: 8
286 taggacgggtg agccgggtcc ctggcccaaa gtgctgctcc ccctccccgt accaaatgct 60
288 gcagaagtaa gagctggtgt cttcgaggct cagggttgctc acagtcagag tggagaacat 120
290 taggggttcgg cggctgatgg gaaacttctc cctggtaaata ccactttcgt aggtggcctc 180
292 tgcaccctgg tttgcggttg caatcagtat caagctctgt cctgggagct gacggtacca 240
294 gaacatcaag gtgacttggg tatcgacctc acagtggatg gtaatggagg tcccacgttg 300
296 acagatgtcc ctgcgcggct tttgagagac aagagctcca aacacagagc cttgtcccag 360
298 gaggagtagc aggcaagtca gcat

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Input Set : E:\2618-102-PUS.ST25.txt

Output Set: N:\CRF4\02232006\I744847A.raw

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301 <210> SEQ ID NO: 9
302 <211> LENGTH: 408
303 <212> TYPE: DNA
304 <213> ORGANISM: Canis familiaris
307 <220> FEATURE:
308 <221> NAME/KEY: CDS
309 <222> LOCATION: (7)..(408)
311 <400> SEQUENCE: 9
312 gctgaa atg gcc acc ggc gtc ttc ttt ggc atg gct ctt tgt gtc ctg      48
313      Met Ala Thr Gly Val Phe Phe Gly Met Ala Leu Cys Val Leu
314      1              5              10
316 tgg aca gga tac atg gat gct gga att atc cag agc cca aga tac aag      96
317 Trp Thr Gly Tyr Met Asp Ala Gly Ile Ile Gln Ser Pro Arg Tyr Lys
318 15              20              25              30
320 gtc aca ggg aca gga aag agg gtg act ctg aga tgt cac cag aca gac      144
321 Val Thr Gly Thr Gly Lys Arg Val Thr Leu Arg Cys His Gln Thr Asp
322              35              40              45
324 aac tat gac tat atg tac tgg tat cga cat gac ctg gga cat ggg ccg      192
325 Asn Tyr Asp Tyr Met Tyr Trp Tyr Arg His Asp Leu Gly His Gly Pro
326              50              55              60
328 agg ctg atc tat tat tca aat ggt att aac agc act gaa aaa gga gac      240
329 Arg Leu Ile Tyr Tyr Ser Asn Gly Ile Asn Ser Thr Glu Lys Gly Asp
330      65              70              75
332 ctc tcc aat gga tac aca gtc tct aga tca aac aag atg gat ttc ccc      288
333 Leu Ser Asn Gly Tyr Thr Val Ser Arg Ser Asn Lys Met Asp Phe Pro
334      80              85              90
336 ctc cta ctg gac tct gtt acc tcc tcc cag aca tct gtg tac ttc tgt      336
337 Leu Leu Leu Asp Ser Val Thr Ser Ser Gln Thr Ser Val Tyr Phe Cys
338 95              100              105              110
340 gcc gac acg agg gat cct gtt gca gta aat tat gat ttt aac ttt ggc      384
341 Ala Asp Thr Arg Asp Pro Val Ala Val Asn Tyr Asp Phe Asn Phe Gly
342              115              120              125
344 cca ggg acc aag ctg aca gtc gta      408
345 Pro Gly Thr Lys Leu Thr Val Val
346      130
349 <210> SEQ ID NO: 10
350 <211> LENGTH: 134
351 <212> TYPE: PRT
352 <213> ORGANISM: Canis familiaris
354 <400> SEQUENCE: 10
356 Met Ala Thr Gly Val Phe Phe Gly Met Ala Leu Cys Val Leu Trp Thr
357 1              5              10              15
360 Gly Tyr Met Asp Ala Gly Ile Ile Gln Ser Pro Arg Tyr Lys Val Thr
361      20              25              30
364 Gly Thr Gly Lys Arg Val Thr Leu Arg Cys His Gln Thr Asp Asn Tyr
365      35              40              45
368 Asp Tyr Met Tyr Trp Tyr Arg His Asp Leu Gly His Gly Pro Arg Leu
369      50              55              60
372 Ile Tyr Tyr Ser Asn Gly Ile Asn Ser Thr Glu Lys Gly Asp Leu Ser

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 02/23/2006
PATENT APPLICATION: US/09/744,847A TIME: 15:00:43

Input Set : E:\2618-102-PUS.ST25.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:60; Xaa Pos. 109
Seq#:61; Xaa Pos. 109,110
Seq#:62; Xaa Pos. 109,110,111
Seq#:63; Xaa Pos. 109
Seq#:64; Xaa Pos. 109,110
Seq#:65; Xaa Pos. 109,110,111
Seq#:66; Xaa Pos. 111
Seq#:67; Xaa Pos. 111,112
Seq#:68; Xaa Pos. 111,112,113
Seq#:69; Xaa Pos. 111
Seq#:70; Xaa Pos. 111,112
Seq#:71; Xaa Pos. 111,112,113
Seq#:72; Xaa Pos. 109
Seq#:73; Xaa Pos. 109,110
Seq#:74; Xaa Pos. 109,110,111
Seq#:75; Xaa Pos. 112
Seq#:76; Xaa Pos. 112,113
Seq#:77; Xaa Pos. 112,113,114
Seq#:78; Xaa Pos. 108
Seq#:79; Xaa Pos. 108,109
Seq#:80; Xaa Pos. 108,109,110
Seq#:81; N Pos. 17
Seq#:101; N Pos. 124,133,138,142,149,151,152,153,154,158,160,162,169,170
Seq#:101; N Pos. 173,177,180,186,193,194,197,204,210,215,218,221,223,224
Seq#:101; N Pos. 225,226,231,236,241,252,253,260,262,265,266,270,273,277
Seq#:101; N Pos. 280,283,286,292,295,306,309,312,332,337,338,340,354,356
Seq#:101; N Pos. 357,358,359,360,361,362
Seq#:102; N Pos. 117,121,124,133,138,142,145,151,157,179,180,182,192,194
Seq#:102; N Pos. 203,206,209,217,218,220,223,231,234,242,251,267,271,272
Seq#:102; N Pos. 274,279,280,282,284,285,287,288,301,302,310,315,318,319
Seq#:102; N Pos. 325,334,343,353,356,358,359,360
Seq#:103; N Pos. 117,149,151,152,167,170,171,176,179,182,184,193,198,199
Seq#:103; N Pos. 201,222,226,236,237,244,249,252,255,262,268,274,276,279
Seq#:103; N Pos. 281,285,287,289,299,300,303
Seq#:104; N Pos. 29,49,51,122,131,137,147,149,151,157,159,177,183,187,189
Seq#:104; N Pos. 192,195,197,198,202,205,213,227,236,237,253,254,255,257
Seq#:104; N Pos. 260,267,271,272,274,279,284,291,293,296,302,305,309,317
Seq#:104; N Pos. 320,321,322,323,324,325,326,327,328,329,330,331,332,333
Seq#:104; N Pos. 334,335,336,337,338,339,340,341,342,343,344,345,346,347
Seq#:104; N Pos. 348,349,350,351,352,353,354,355,356,357
Seq#:105; N Pos. 124,136,142,159,162,173,176,182,185,187,197,201,202,212
Seq#:105; N Pos. 221,227,230,241,251,254,259,261,264,268,270,275,277,278
Seq#:105; N Pos. 281,284,295,299,313,315,324
Seq#:106; N Pos. 1,3,15,23,128,140,146,152,156,158,159,161,162,166,167,168

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Seq#:106; N Pos. 170,171,173,174,175,177,187,195,197,198,200,202,203,205
Seq#:106; N Pos. 206,213,216,218,221,226,232,239,241,246,247,255,257,258
Seq#:106; N Pos. 261,266,273,276,280,283,288,291,299,319,320,322,325,326
Seq#:106; N Pos. 330,336,339,342,344,346,347,349,350,352,353,356
Seq#:107; N Pos. 132,135,138,148,151,152,160,167,168,181,183,189,191,192
Seq#:107; N Pos. 193,204,208,214,221,222,224,232,233,241,243,244,246,253
Seq#:107; N Pos. 255,262,272,281,283,288,289,293,300,301,304,307,308,310

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:50,51,52,53,54,55,56,57,58,59,81,82,83,84,85,86,87,88,89,90,91,92,93,94
Seq#:95,96,97

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Input Set : E:\2618-102-PUS.ST25.txt

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L:1887 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:60 after pos.:96
 L:1928 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:61 after pos.:96
 L:1969 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:62 after pos.:96
 L:2010 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:63 after pos.:96
 L:2051 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:64 after pos.:96
 L:2092 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:65 after pos.:96
 L:2133 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66 after pos.:96
 L:2174 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:67 after pos.:96
 L:2215 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:68 after pos.:96
 M:341 Repeated in SeqNo=68
 L:2260 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:69 after pos.:96
 L:2301 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:70 after pos.:96
 L:2342 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:71 after pos.:96
 M:341 Repeated in SeqNo=71
 L:2387 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:72 after pos.:96
 L:2428 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:73 after pos.:96
 L:2469 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:74 after pos.:96
 L:2510 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:75 after pos.:96
 L:2551 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:76 after pos.:96
 M:341 Repeated in SeqNo=76
 L:2596 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:77 after pos.:96
 M:341 Repeated in SeqNo=77
 L:2641 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:78 after pos.:96
 L:2682 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:79 after pos.:96
 L:2723 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:80 after pos.:96
 L:2742 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:81 after pos.:0
 L:3287 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:101 after pos.:120
 M:341 Repeated in SeqNo=101
 L:3507 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:102 after pos.:60
 M:341 Repeated in SeqNo=102
 L:3677 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:103 after pos.:60
 M:341 Repeated in SeqNo=103
 L:3890 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:104 after pos.:0
 M:341 Repeated in SeqNo=104
 L:4079 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:105 after pos.:120
 M:341 Repeated in SeqNo=105
 L:4360 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:106 after pos.:0
 M:341 Repeated in SeqNo=106
 L:4576 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:107 after pos.:120
 M:341 Repeated in SeqNo=107
 L:4774 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:108 after pos.:0
 M:341 Repeated in SeqNo=108
 L:4841 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:109 after pos.:0
 M:341 Repeated in SeqNo=109
 L:5091 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:110 after pos.:0
 M:341 Repeated in SeqNo=110
 L:5276 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:111 after pos.:0
 M:341 Repeated in SeqNo=111